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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/824,735

DATE: 09/07/2001  
 TIME: 14:11:35

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3 <110> APPLICANT: ZHU, JIAN-KANG  
 4 LIU, JIPING  
 5 ISHITANI, MANABU  
 6 HALFTER, URSULA  
 7 KIM, CHEOL-SOO  
 9 <120> TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS  
 11 <130> FILE REFERENCE: 205645US20  
 13 <140> CURRENT APPLICATION NUMBER: 09/824,735  
 C--> 14 <141> CURRENT FILING DATE: 2001-08-17  
 16 <150> PRIOR APPLICATION NUMBER: US 60/824,735  
 17 <151> PRIOR FILING DATE: 2000-04-04  
 19 <160> NUMBER OF SEQ ID NOS: 16  
 21 <170> SOFTWARE: PatentIn version 3.1  
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 25 <212> TYPE: DNA  
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 111 cgggaaaatc acggatttat gtttttttgtt gaaaaattaa cgagttact tttctcaat 180  
 113 ttcattgctt gtatatttaa gaaatttgaa aaaatattaa ttttattaaa ttgttttaga 240  
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 121 tcaaaaattt caactcatta gggttcatgg gttgagttga gttgagttga cccatgaatt 480  
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163	caattctgg	atttcacat	tctcttcga	ctacgccccaa	tcgcaattcc	agccgtacga	1740
165	attttatata	ttgattatga	tcttgatcct	tacctttcg	tcgtttcctt	gatcgaattt	1800
167	atgttgattt	atgctgcgaa	atcaaattta	tggatacaga	gtaattttgt	atatatggat	1860
169	gtgttaggagc	taaaatttagc	aaacaatacg	taaagtaatt	gaaatcgaaa	tcataaacgt	1920
171	ttaaggaaag	aggttttac	taagtctctg	aataatctga	ttgatagctt	gtggtaatg	1980
173	gatcagataa	aagtttgtaa	aga	atg aca aag	aaa atg aga	gtg ggc aag	2033
174				Met Thr Lys Lys	Met Arg Arg	Val Gly Lys	
175				1	5	10	
177	tac gag gtt	ggt cgc aca	ata ggt gaa	gga acc ttt	gct aag gtt	aag	2081
178	Tyr Glu Val	Gly Arg Thr	Ile Gly Glu	Gly Thr Phe	Ala Lys Val	Lys	
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181	ttt gcg agg	aac aca gac	act ggt gat	aat gta gcc	atc aaa att	atg	2129
182	Phe Ala Arg	Asn Thr Asp	Thr Gly Asp	Asn Val Ala	Ile Lys Ile	Met	
183				30	35	40	
185	gct aag agt	aca ata ctt	aag aac aga	atg gtt gat	cag gtatgttctg		2178
186	Ala Lys Ser	Thr Ile Leu	Lys Asn Arg	Met Val Asp	Gln		
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191	taaagcttt	ttacag ata	aaa aga	gag ata tct	ata atg aag	att gtt cgt	2290
192				Ile Lys Arg	Glu Ile Ser	Ile Met Lys Ile Val Arg	
193					60	65	
195	cac ccg aac	ata gtg agg	ttg tat	gag gtatgttctt	ttgtttccat		2337
196	His Pro Asn	Ile Val Arg	Leu Tyr Glu				
197				70	75		
199	gcatctgcga	aattttatct	ctgaagtgtt	tttgcacat	tgttcttcgt	ttgttttttt	2397
201	gtgattttcc	cgatgttag	gtg ttg	gct agt cct tcg	aaa ata tat	ata gtt	2448
202				Val Leu Ala	Ser Pro Ser	Lys Ile Tyr Ile Val	
203					80	85	
205	ttg gag ttt	gtg aca gga	gga gag	ctc ttt	gat aga	att gtacggact	2497
206	Leu Glu Phe	Val Thr Gly	Gly Glu Leu	Phe Asp Arg	Ile		
207				90	95	100	
209	tccataacttg	taggcagcgt	ccattagttt	aaacctctct	acttaatttt	ttaatataatg	2557
211	aaatctttca	tgcag gtt	cat aaa	ggg agg ctt	gaa gaa	agt gag tct cgg	2608
212				Val His Lys	Gly Arg Leu	Glu Glu Ser Arg	
213					105	110	
215	aaa tac ttt	caa cag ctt	gta gat	gct gtt	gct cat	tgt cac tgc aag	2656
216	Lys Tyr Phe	Gln Gln Leu	Val Asp Ala	Val Ala His	Cys His	Cys Lys	
217				115	120	125	
219	ggt gtt tac	cac cgt gac	cta aag	gtaaagacgt	gtttttgtt	accaatattc	2710
220	Gly Val Tyr	His Arg Asp	Leu Lys				
221				130	135		
223	ctcagaatat	ctcaactgcgt	tgcaatccag	acttgatatt	tttgcgtcgc	tatgttatgt	2770
225	tatcttag	cca gaa aat	ctt tta ctc	gat aca aat	gga aat ctg	aag gtt	2819
226				Pro Glu Asn	Leu Leu Asp	Thr Asn Gly Asn Leu Lys Val	
227					140	145	150
229	tcg gat ttc	gga ctc	agt gca	ttg cct cag	gaa gtaagtgc	ttatctctgc	2872
230	Ser Asp Phe	Gly Leu	Ser Ala	Leu Pro	Gln Glu		

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238	Leu	Leu	Arg	Thr	Thr	Cys	Gly	Thr	Pro	Asn	Tyr	Val	Ala	Pro	Glu	Val				
239	165						170				175					180				
241	ctt	agt	gga	cag	ggt	tac	gat	ggt	tca	gca	gct	gat	att	tgg	tct	tgc	3025			
242	Leu	Ser	Gly	Gln	Gly	Tyr	Asp	Gly	Ser	Ala	Ala	Asp	Ile	Trp	Ser	Cys				
243							185				190					195				
245	ggg	gtt	att	ctt	ttc	gtt	ata	ttg	gct	gga	tat	tta	cct	ttt	tcc	gag	3073			
246	Gly	Val	Ile	Leu	Phe	Val	Ile	Leu	Ala	Gly	Tyr	Leu	Pro	Phe	Ser	Glu				
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261							230				235					240				
263	cat	agg	ata	ctt	gac	ccc	aat	ccc	aaa	aca	gtgag	tattt	tgctttgttc				3334			
264	His	Arg	Ile	Leu	Asp	Pro	Asn	Pro	Lys	Thr										
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274	Pro	Trp	Phe	Arg	Leu	Asn	Tyr	Val	Pro	Ile	Arg	Ala	Arg	Glu	Glu					
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277	gaa	gtg	aat	ttg	gat	att	cgt	gca	gtt	ttt	gat	gga	att	gag		3540				
278	Glu	Val	Asn	Leu	Asp	Asp	Ile	Arg	Ala	Val	Phe	Asp	Gly	Ile	Glu					
279							280				285					290				
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319 gat ttt gtt aaa agg caa acc cgt ttt gtt tct cga agg gaa cct agt	4447
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324 Glu Ile Ile Ala Asn Ile Glu Ala Val Ala Asn Ser Met Gly Phe Lys	
325 350 355 360	
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328 Ser His Thr Arg Asn Phe Lys	
329 365 370	
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335 gaatttatcat tttaatgtt agcagagat acaattgtt tgatttggta cgtctatgtg	4726
337 ctcaacag aca agg ctc gag gga tta tct tcg atc aag gcc gga cag tta	4776
338 Thr Arg Leu Glu Gly Leu Ser Ser Ile Lys Ala Gly Gln Leu	
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342 Ala Val Val Ile Glu	
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346 Ile Tyr Glu	
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354 Thr Leu Glu Tyr His Lys	
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